```
            RAW SEQUENCE LISTING                DATE: 11/20/2000
            PATENT APPLICATION:  US/09/699,652  TIME: 20:20:55

            Input Set : A:\Pto.amc
            Output Set: N:\CRF3\11202000\I699652.raw

    ·2 <110> APPLICANT: Cahoon, Edgar B.
     3          Cahoon, Rebecca E.
     4          Kinney, Anthony J.
     5          Rafalski, J. Antoni
     7 <120> TITLE OF INVENTION: TRIACYLGLYCEROL LIPASES
     9 <130> FILE REFERENCE: BB1168 US NA
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/699,652
C--> 12 <141> CURRENT FILING DATE: 2000-10-30
    14 <150> PRIOR APPLICATION NUMBER: 60/083,688
    15 <151> PRIOR FILING DATE: 1988-04-30
    17 <150> PRIOR APPLICATION NUMBER: PCT/US99/09280
    18 <151> PRIOR FILING DATE: 1999-04-29
    20 <160> NUMBER OF SEQ ID NOS: 36
    22 <170> SOFTWARE: Microsoft Office 97
    24 <210> SEQ ID NO: 1
    25 <211> LENGTH: 751
    26 <212> TYPE: DNA
    27 <213> ORGANISM: Zea mays
    29 <400> SEQUENCE: 1
    30 gcacgagatc accggcaaga actactgcct caacagctcc gccgtcgacg tcttcctcaa   60
    31 gtacgagccc cagccgacct ccaccaaaac catggtccac ttcgctcaaa ccgtgcgcga  120
    32 cggcgtgctg accaagtacg actacgtgct gccggagcgg aacatcgcca gctacggcca  180
    33 ggccgagccg ccggtgtacc ggatgtccgg catcccgccg agcttcccgc tcttcctcag  240
    34 ctacggcggc cgggactcgc tcgccgaccc cgccgacgtg cgcctcctcc tgcaggacct  300
    35 ccggggccac gaccaggaca agctcacggt gcagtacctg gacaagttcg cgcacctcga  360
    36 cttcatcatc ggcgtctgcg ccaaggacta cgtctacaag gacatgatcg acttcctaaa  420
    37 ccgcttcaac tagtactagc atatatattt gcttcaatcg gtgtcgtctt cagccccagc  480
    38 aggattagac aaaaaaaggg ggggacactg cagctcgtaa acgttgtcca tacagattat  540
    39 cagaggtgaa aaccatacat gatgtaattt agcattagat agttaaaaca tggagctgcc  600
    40 tcagtatgga ggattgtcaa ctactctcca tcacagcagt aggtgtgatg tagaagagtg  660
    41 attgtcacac tgtgtgtgtt gcaaatttgc aacacagtga ttactaatat aaaaaatact  720
    42 cttgagttaa aaaaaaaaaa aaaaaaaaaa a                                 751
    44 <210> SEQ ID NO: 2
    45 <211> LENGTH: 143
    46 <212> TYPE: PRT
    47 <213> ORGANISM: Zea mays
    49 <400> SEQUENCE: 2
    50 His Glu Ile Thr Gly Lys Asn Tyr Cys Leu Asn Ser Ser Ala Val Asp
    51  1               5                  10                  15
    53 Val Phe Leu Lys Tyr Glu Pro Gln Pro Thr Ser Thr Lys Thr Met Val
    54              20                  25                  30
    56 His Phe Ala Gln Thr Val Arg Asp Gly Val Leu Thr Lys Tyr Asp Tyr
    57          35                  40                  45  ·
    59 Val Leu Pro Glu Arg Asn Ile Ala Ser Tyr Gly Gln Ala Glu Pro Pro
    60          50                  55                  60
    62 Val Tyr Arg Met Ser Gly Ile Pro Pro Ser Phe Pro Leu Phe Leu Ser
    63  65                  70                  75                  80
```

```
65 Tyr Gly Gly Arg Asp Ser Leu Ala Asp Pro Ala Asp Val Arg Leu Leu
66              85              90                       95
68 Leu Gln Asp Leu Arg Gly His Asp Gln Asp Lys Leu Thr Val Gln Tyr
69              100             105             110
71 Leu Asp Lys Phe Ala His Leu Asp Phe Ile Ile Gly Val Cys Ala Lys
72          115             120             125
74 Asp Tyr Val Tyr Lys Asp Met Ile Asp Phe Leu Asn Arg Phe Asn
75      130             135             140
77 <210> SEQ ID NO: 3
78 <211> LENGTH: 647
79 <212> TYPE: DNA
80 <213> ORGANISM: Catalpa sp.
82 <400> SEQUENCE: 3
83 ttatctttca ggagagattt ttgtttgaat gctcccccg ttgagctttt tgtggaaaat  60
84 taccctccat cttccgtgaa ttgagacccc tgtccatatg gctcaaactg tccgatatgg 120
85 gatcctaccc aaatacgact acggcaatcc cagcttcaac ttggcccatt atggtgaatc 180
86 cagacctccc gtttacgatt tatccaagat tcccctcgac attccgctct tcctaagcta 240
87 tggaggacaa gatgcattgt cggatgttaa ggatgtcgag acattgctcg atagtctcaa 300
88 gttacacgat gtggataagc tgcatgtgca gtatatcaag gattatgctc atgccgactt 360
89 cattatcgga gttactgcaa aagatatagt ttataatcag attgtaactt ttttcagaaa 420
90 ccaggcttga gaggttcttg attttggagt gcttttgctg tgagaatgca acagcttgtt 480
91 ccactcttgt tgaatgtgaa taagccattt ccgagagatt taatggctgg taaagcttat 540
92 tagtttactc atagatacat gtaagaagca acccgataca tagtttgaat cctttatctc 600
93 gaaaaggtat tgcatctcct cttctacgtc aaaaaaaaaa aaaaata          647
95 <210> SEQ ID NO: 4
96 <211> LENGTH: 116
97 <212> TYPE: PRT
98 <213> ORGANISM: Catalpa sp.
100 <400> SEQUENCE: 4
101 Ile Glu Thr Pro Val His Met Ala Gln Thr Val Arg Tyr Gly Ile Leu
102   1               5               10                      15
104 Pro Lys Tyr Asp Tyr Gly Asn Pro Ser Phe Asn Leu Ala His Tyr Gly
105              20              25              30
107 Glu Ser Arg Pro Pro Val Tyr Asp Leu Ser Lys Ile Pro Leu Asp Ile
108          35              40              45
110 Pro Leu Phe Leu Ser Tyr Gly Gly Gln Asp Ala Leu Ser Asp Val Lys
111      50              55              60
113 Asp Val Glu Thr Leu Leu Asp Ser Leu Lys Leu His Asp Val Asp Lys
114  65              70              75                      80
116 Leu His Val Gln Tyr Ile Lys Asp Tyr Ala His Ala Asp Phe Ile Ile
117              85              90              95
119 Gly Val Thr Ala Lys Asp Ile Val Tyr Asn Gln Ile Val Thr Phe Phe
120              100             105             110
122 Arg Asn Gln Ala
123          115
125 <210> SEQ ID NO: 5
126 <211> LENGTH: 705
127 <212> TYPE: DNA
128 <213> ORGANISM: Catalpa sp.
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130 <220> FEATURE:
131 <221> NAME/KEY: unsure
132 <222> LOCATION: (526)
134 <220> FEATURE:
135 <221> NAME/KEY: unsure
136 <222> LOCATION: (561)
138 <220> FEATURE:
139 <221> NAME/KEY: unsure
140 <222> LOCATION: (585)
142 <220> FEATURE:
143 <221> NAME/KEY: unsure
144 <222> LOCATION: (593)
146 <220> FEATURE:
147 <221> NAME/KEY: unsure
148 <222> LOCATION: (664)
150 <220> FEATURE:
151 <221> NAME/KEY: unsure
152 <222> LOCATION: (679)
154 <400> SEQUENCE: 5
155 gcacgagcca acagcttcct aaatttagct cttctaatcc ttctctcatt atcactactc  60
156 ctacctcatc aatcattcgc ctccagccgc cgccgttttc ttccgcagaa tgatgtcgtt 120
157 cttccgccgg acggcgtttg ctccaccgcc gtaactgtac acggttataa atgccaagaa 180
158 tttgaagtaa cgactgatga tggctatata ttaagcgtgc agaggattct ggagggccgg 240
159 gccggaggag gaggccgaa gcgccgccg gttctgctgc aacatggggt tcttgtggac 300
160 gggatgacgt ggctggtgaa tggaccggaa caatctttgg cgatgatatt ggctgacaat 360
161 gggttcgacg tctggatttc taacataaga ggaactaggt ttagtcgtcg tcatgtcagc 420
162 cttgatccta ccgatcctga atattgggat tgggcatggg acgatcttgg tgacccacga 480
W--> 163 cttaccatcc ctgatcgagt tagtggtcag acaaacgggt cagaaacac actacatagg 540
W--> 164 gcaatccatg gggaacttta ntagctttgg gatcactttt aggangaaa cangttggca 600
165 gggtaaatcg gctgtatgt aagccaattg gctaacgagt catatgcaac tgctctcgag 660
W--> 166 ttgnctagca gatccttgnt ggggaacaca cgatcttggc ctgcg            705
168 <210> SEQ ID NO: 6
169 <211> LENGTH: 157
170 <212> TYPE: PRT
171 <213> ORGANISM: Catalpa sp.
173 <400> SEQUENCE: 6
174 Ala Arg Ala Asn Ser Phe Leu Asn Leu Ala Leu Leu Ile Leu Leu Ser
175  1               5              10               15
177 Leu Ser Leu Leu Leu Pro His Gln Ser Phe Ala Ser Ser Arg Arg Arg
178          20              25               30
180 Phe Leu Pro Gln Asn Asp Val Val Leu Pro Pro Asp Gly Val Cys Ser
181          35              40               45
183 Thr Ala Val Thr Val His Gly Tyr Lys Cys Gln Glu Phe Glu Val Thr
184      50              55              60
186 Thr Asp Asp Gly Tyr Ile Leu Ser Val Gln Arg Ile Leu Glu Gly Arg
187 65              70              75              80
189 Ala Gly Gly Gly Gly Pro Lys Arg Pro Pro Val Leu Leu Gln His Gly
190              85              90               95
192 Val Leu Val Asp Gly Met Thr Trp Leu Val Asn Gly Pro Glu Gln Ser
```

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          Input Set : A:\Pto.amc
          Output Set: N:\CRF3\11202000\I699652.raw

  193              100              105              110
  195 Leu Ala Met Ile Leu Ala Asp Asn Gly Phe Asp Val Trp Ile Ser Asn
  196         115              120              125
  198 Ile Arg Gly Thr Arg Phe Ser Arg Arg His Val Ser Leu Asp Pro Thr
  199     130              135              140
  201 Asp Pro Glu Tyr Trp Asp Trp Ala Trp Asp Asp Leu Gly
  202 145              150              155
  204 <210> SEQ ID NO: 7
  205 <211> LENGTH: 859
  206 <212> TYPE: DNA
  207 <213> ORGANISM: Zea mays
  209 <220> FEATURE:
  210 <221> NAME/KEY: unsure
  211 <222> LOCATION: (46)
  213 <220> FEATURE:
  214 <221> NAME/KEY: unsure
  215 <222> LOCATION: (231)
  217 <400> SEQUENCE: 7
W--> 218 aaagcaaaca acggcggaca tggtgcgccc aggaaaagcg cttgcngcgc cccagctcct  60
  219 cctcctcgtg ttcctctgcc tcctagccgg tggagcccgc gcatccccgc ccacagacgc 120
  220 gctacgccgc gtctccccgc gcgcgggggc cggtggcctc tgccagcagc tyctcctgcc 180
W--> 221 gcaggttacc cgtgcaccga gcacaccgtt caaacggatg atggctttct nttgtctctt 240
  222 cagcatattc cacatggcag aaatggaatt gcagataata ctggacctcc agttttttctt 300
  223 cagcacggtc ttttccaggg tggagataca tggttcataa actccaatga acaatcactt 360
  224 ggatatatcc ttgctgacaa tggtttttgat gtttgggtcg gaaatgttcg tggcacacgt 420
  225 tggagtaaag gccactctac tctctctgtt catgataagc tttttctggga ttggagttgg 480
  226 caagaccttg ctgaatacga cgttttggca atgttaagct atgtatatac agttgcacag 540
  227 tccaaaattt tgtatgtggg acattcacag ggaactatca tgggtttggc tgcgtttaca 600
  228 atgcctgaaa cagtaaagat gataagctct gctgcgcttc tttgtcccat ttcttacctt 660
  229 gatcacgtca gtgctagttt tgttcttaga gcagttgcca tgcatcttga tgagatgctt 720
  230 gttattatgg gcatccatca gttgaacttc cggagcgata tgggtgtaca gatattagat 780
  231 tcgctgtgcg atgatgaaca tttggactgc aacgatctgt tatcttcaat aacagtcaaa 840
  232 actgttgttc aatcatctc                                              859
  234 <210> SEQ ID NO: 8
  235 <211> LENGTH: 286
  236 <212> TYPE: PRT
  237 <213> ORGANISM: Zea mays
  239 <220> FEATURE:
  240 <221> NAME/KEY: UNSURE
  241 <222> LOCATION: (16)
  243 <400> SEQUENCE: 8
W--> 244 Lys Ala Asn Asn Gly Gly His Gly Ala Pro Arg Lys Ser Ala Cys Xaa
  245  1               5               10               15
  247 Ala Pro Ala Pro Pro Pro Arg Val Pro Leu Pro Pro Ser Arg Trp Ser
  248             20              25              30
  250 Pro Arg Ile Pro Ala His Arg Arg Ala Thr Pro Arg Leu Pro Ala Arg
  251         35              40              45
  253 Gly Gly Arg Trp Pro Leu Pro Ala Ala Ala Pro Ala Ala Gly Tyr Pro
  254     50              55              60
```

```
256 Cys Thr Glu His Thr Val Gln Thr Asp Asp Gly Phe Leu Leu Ser Leu
257 65                      70                  75                 80
259 Gln His Ile Pro His Gly Arg Asn Gly Ile Ala Asp Asn Thr Gly Pro
260                 85                  90              95
262 Pro Val Phe Leu Gln His Gly Leu Phe Gln Gly Gly Asp Thr Trp Phe
263             100             105             110
265 Ile Asn Ser Asn Glu Gln Ser Leu Gly Tyr Ile Leu Ala Asp Asn Gly
266         115             120             125
268 Phe Asp Val Trp Val Gly Asn Val Arg Gly Thr Arg Trp Ser Lys Gly
269     130             135             140
271 His Ser Thr Leu Ser Val His Asp Lys Leu Phe Trp Asp Trp Ser Trp
272 145             150             155                 160
274 Gln Asp Leu Ala Glu Tyr Asp Val Leu Ala Met Leu Ser Tyr Val Tyr
275             165             170             175
277 Thr Val Ala Gln Ser Lys Ile Leu Tyr Val Gly His Ser Gln Gly Thr
278             180             185             190
280 Ile Met Gly Leu Ala Ala Phe Thr Met Pro Glu Thr Val Lys Met Ile
281         195             200             205
283 Ser Ser Ala Ala Leu Leu Cys Pro Ile Ser Tyr Leu Asp His Val Ser
284     210             215             220
286 Ala Ser Phe Val Leu Arg Ala Val Ala Met His Leu Asp Glu Met Leu
287 225             230             235                 240
289 Val Ile Met Gly Ile His Gln Leu Asn Phe Arg Ser Asp Met Gly Val
290             245             250             255
292 Gln Ile Leu Asp Ser Leu Cys Asp Asp Glu His Leu Asp Cys Asn Asp
293         260             265             270
295 Leu Leu Ser Ser Ile Thr Val Lys Thr Val Val Gln Ser Ser
296         275             280             285
298 <210> SEQ ID NO: 9
299 <211> LENGTH: 509
300 <212> TYPE: DNA
301 <213> ORGANISM: Zea mays
303 <220> FEATURE:
304 <221> NAME/KEY: unsure
305 <222> LOCATION: (162)
307 <220> FEATURE:
308 <221> NAME/KEY: unsure
309 <222> LOCATION: (277)
311 <220> FEATURE:
312 <221> NAME/KEY: unsure
313 <222> LOCATION: (284)
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316 <221> NAME/KEY: unsure
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319 <220> FEATURE:
320 <221> NAME/KEY: unsure
321 <222> LOCATION: (295)
323 <220> FEATURE:
324 <221> NAME/KEY: unsure
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FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 11/20/2000
PATENT APPLICATION: US/09/699,652   TIME: 20:20:56

          Input Set : A:\Pto.amc
          Output Set: N:\CRF3\11202000\I699652.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:163 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:163 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:164 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:166 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:218 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:218 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:221 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
M:340 Repeated in SeqNo=7
L:244 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:244 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:354 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:354 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:356 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
M:340 Repeated in SeqNo=9
L:358 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:359 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:360 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:393 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:393 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
L:399 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
M:340 Repeated in SeqNo=10
L:442 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:442 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:445 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
M:340 Repeated in SeqNo=11
L:446 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:486 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:486 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
L:489 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
M:340 Repeated in SeqNo=12
L:682 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:682 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:683 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
M:340 Repeated in SeqNo=15
L:685 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:686 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:687 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:688 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:712 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:712 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:721 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
M:340 Repeated in SeqNo=16
L:1058 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:1058 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23
L:1060 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23

VERIFICATION SUMMARY   DATE: 11/20/2000
PATENT APPLICATION: US/09/699,652   TIME: 20:20:56

Input Set : A:\Pto.amc
Output Set: N:\CRF3\11202000\I699652.raw

M:340 Repeated in SeqNo=23
L:1062 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:1076 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:1077 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:1107 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24
L:1107 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24
L:1110 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24
M:340 Repeated in SeqNo=24
L:1122 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24
L:1175 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1175 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
L:1208 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1208 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26
L:1299 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1299 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27
L:1300 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
M:340 Repeated in SeqNo=27